



Title: NUCLEIC SEQUENCES CODING FOR AN AT2 INTERACTING  
PROTEIN INTERACTING WITH THE AT2 RECEPTOR ...

Inventor(s): Elbaz et al.

Application No: 09/762,194

Notice of Allowance Dated July 15 2004

Atty Dkt No: 033339/208804

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LOCUS

AT2 receptor C-terminal end

160 BP DS-DNA

ORGANISM Mouse

BASES

41 A

33 C

36 G

50 T

Nucleic acids

```
1 TGTGTTAATC CCTTCCTGTA TTGTTTTGTT GGAAACCGCT
  TCCAACAGAA CGTCCGCAGT GTGTTTAGAG TTCCCATTAC
  TTGGCTCCAA GGCAAGAGAG AGACTATGTC TTGCAGAAAA
121 GGCAGTTCTC TTAGAGAAAT GGACACCTTT GTGTCTTAAA
```

Translation into amino acids

```
CVNPFLYCFV GNRFQQNVRS VFRVPITWLQ GKRETMSCRK
GSSLREMDTFVS•
```

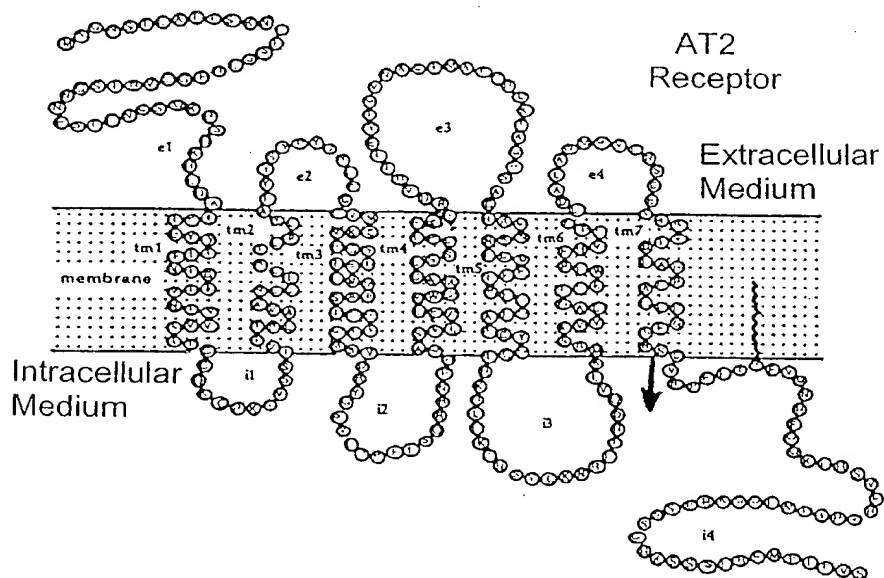


Figure 1



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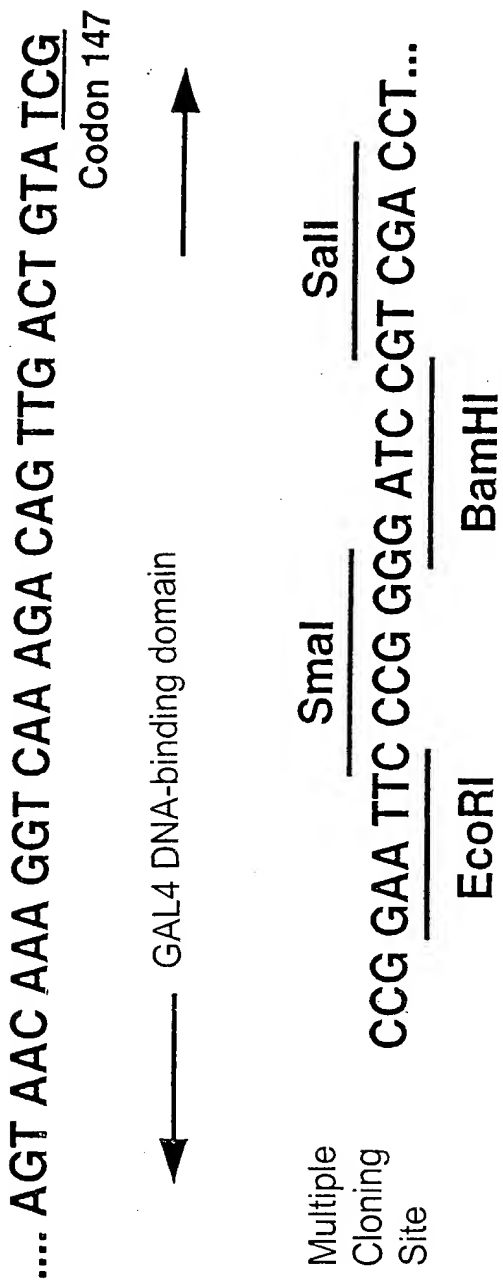


Figure 2

Title: NUCLEIC SEQUENCES CODING FOR AN AT2 INTERACTING  
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GCTACCCCCCCCCACGCACCCCCCAATCTGGGTGGCCTGGCATTAGCATGTAAGCTTGTTTTCTCTGGC	71
TGTATCTCTTGGCCTGGAAGAACCCCGAGTTGCCAAGAGACACAGTATGTGATGGTCCCTGGAAAAGCTGCT	143
TCCCCTGCGAAGTTCTCCCACTGGCTTCGAAGAC	9
ATG CTG TTG TCT CCC AAA TTC TCC TTA	204
S T I H V R L T A K G L L R N L R L	27
TCC ACC ATC CAC GTC CGC CTA ACC GCC AAA GGA CTG CTT CGA AAC CTC CGG CTT	258
P S G L R K N T V I F H T V E K G R	45
CCT TCG GGG CTC AGG AAA AAC ACT GTC ATT TTC CAC ACA GTT GAA AAG GGC AGG	312
Q K N P R S L C I Q T Q T A P D V L	63
CAG AAG AAT CCC AGG AGC CTG TGC ATC CAG ACC CAG ACA GCT CCA GAT GTG CTG	366
S S E R T L E L A Q Y K T K C E S Q	81
TCC TCC GAG AGA ACG CTT GAG TTG GCC CAA TAC AAG ACA AAA TGT GAA AGC CAA	420
S G F I L H L R Q L L S R G N N K F	99
AGT GGA TTC ATC CTG CAC CTC AGG CAG CTT CTT TCC CGT GGT AAC AAC AAG TTT	474
E A L T V V I Q H L L S E R E E A L	117
GAA GCG CTG ACA GTT GTG ATC CAG CAC CTC CTG TCT GAG CGG GAG GAA GCA CTG	528
K Q H K T L S Q E L V S L R G E L V	135
AAG CAA CAC AAA ACC CTC TCT CAA GAA CTT GTC AGC CTC CGG GGA GAG CTA GTT	582
A A S S A C E K L E K A R A D L Q T	153
GCT GCT TCA AGC GCC TGT GAG AAG CTA GAA AAG GCT AGG GCT GAC TTA CAG ACA	636
A Y Q E F V Q K L N Q Q H Q T D R T	171
GCG TAT CAA GAA TTT GTC CAG AAA CTA AAC CAG CAG CAT CAG ACA GAC CGG ACG	690
E L E N R L K D L Y T A E C E K L Q	189
GAA CTG GAG AAC CGG CTG AAG GAC TTA TAC ACC GCA GAG TGT GAG AAG CTT CAG	744
S I Y I E E A E K Y K T Q L Q E Q F	207
AGC ATT TAC ATT GAG GAG GCA GAA AAA TAT AAA ACT CAA CTG CAA GAG CAG TTT	798
D N L N A A H E T T K L E I E A S H	225
GAC AAC TTA AAC GCC GCC CAT GAG ACC ACT AAG CTT GAG ATT GAA GCT AGC CAC	852
S E K V E L L K K T Y E T S L S E I	243
TCG GAG AAG GTG GAA TTG CTG AAG AAG ACC TAT GAA ACC TCC CTT TCA GAA ATC	906
K K S H E M E K K S L E D L L N E K	261
AAG AAG AGC CAT GAG ATG GAG AAG AAG TCA CTG GAG GAT CTG CTT AAT GAG AAG	960
Q E S L E K Q I N D L K S E N D A L	279
CAG GAA TCG CTG GAG AAA CAA ATC AAT GAT CTG AAG AGT GAA AAC GAT GCT TTA	1014
N E R L K S E E Q K Q L S R E K A N	297
AAC GAA AGG TTG AAA TCA GAG GAG CAA AAG CAA CTG TCA AGA GAG AAG GCG AAT	1068
S K N P Q V M Y L E Q E L E S L K A	315
TCC AAA AAC CCT CAG GTC ATG TAT CTG GAG CAA GAA CTA GAA AGC CTG AAG GCT	1122

**Figure 3.1**



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V	L	E	I	K	N	E	K	L	H	Q	Q	D	M	K	L	M	K	333
GTG	TTA	GAG	ATC	AAG	AAT	GAG	AAG	CTG	CAC	CAG	CAG	GAC	ATG	AAG	CTA	ATG	AAG	1176
M	E	K	L	V	D	N	N	T	A	L	V	D	K	L	K	R	F	351
ATG	GAA	AAG	CTG	GTG	GAC	AAT	AAC	ACA	GCA	TTG	GTT	GAC	AAG	CTG	AAG	CGA	TTC	1230
Q	Q	E	N	E	E	L	K	A	R	M	D	K	H	M	A	I	S	369
CAG	CAG	GAA	AAC	GAG	GAG	TTA	AAA	GCT	CGC	ATG	GAC	AAA	CAC	ATG	GCA	ATT	TCA	1284
R	Q	L	S	T	E	Q	A	A	L	Q	E	S	L	E	K	E	S	387
AGG	CAA	CTT	TCC	ACC	GAG	CAG	GCC	GCG	CTG	CAA	GAG	TCC	CTT	GAG	AAG	GAG	TCA	1338
K	V	N	K	R	L	S	M	E	N	E	E	L	L	W	K	L	H	405
AAG	GTC	AAC	AAG	AGA	CTG	TCC	ATG	GAG	AAC	GAG	GAA	CTT	CTG	TGG	AAA	CTG	CAC	1392
N	G	D	L	C	S	P	K	R	S	P	T	S	S	A	I	P	F	423
AAC	GGA	GAC	CTG	TGC	AGC	CCC	AAG	AGA	TCC	CCC	ACC	TCC	TCG	GCC	ATC	CCT	TTC	1446
Q	S	P	R	N	S	G	S	F	S	S	P	S	I	S	P	R	*	440
CAG	TCC	CCC	AGG	AAT	TCT	GGT	TCC	TTC	TCC	AGC	CCC	AGC	ATC	TCA	CCC	AGA	TGA	1500
CGGCTTCTGAACGCAGGAGACTCTCTGAAGGCACTGAGGTGCGCTTCTGCAGGACTGACCCTCTCATGGGA	1571																	
ACTCGAGTTGCTGCGTTAGCTCTCTGGAATATCCCCAGGATATCGGGAGAGCAGCCGCCAACCGTATCAGC	1642																	
TACGTACGAATAGAGAGCTCCAATAGAAGACTTTTAACTTGGTCCAAAAGCCTCCTCCAAAAACAGATTTTC	1713																	
GGAAGTGAAGTGGACATAGTTGCACAAAGCACTTACGGAACGAGGGAACCTTGTTCTTTGCCTTCCTTCAC	1784																	
CTAAGCATAGGCTTTCCAG	1803																	

**Figure 3.2**



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cagtgtgatgtggttcagaggcagcttctagacctgcaggagggagattgtattcagaggaagagcatcatt	72
ttggcaacatctgaaagtgaaaacggaagccagaaacacttggccagccctgggggatttttttcttctatg	144
cctctgtggttggaaatgacatttctgtgtgtagcatctttctctgactgtatttcttggccttgaagagtac	216
tgagtttaaaaagacagtatgtgacagtccatggaaattgcctcttctgtgaaatctcgccacctgctccga	288
agac ATG TTG TTG TCT CCC AAA TTC TCC TTA TCC ACC ATT CAC ATA CGA CTG ACG	343
M L L S P K F S L S T I H I R L T	17
GCC AAA GGA TTG CTT CGA AAC CTT CGA CTT CCT TCA GGG TTT AGG AGA AGC ACT	397
A K G L L R N L R L P S G F R R S T	35
GTT GTT TTC CAC ACA GTT GAA AAG AGC AGG CAA AAG AAT CCT CGA AGC TTA TGT	451
V V F H T V E K S R Q K N P R S L C	53
ATC CAG CCA CAG ACA GCT CCC GAT GCG CTG CCC CCT GAG AAA ACA CTT GAA TTG	505
I Q P Q T A P D A L P P E K T L E L	71
ACG CAA TAT AAA ACA AAA TGT GAA AAC CAA AGT GGA TTT ATC CTG CAG CTC AAG	559
T Q Y K T K C E N Q S G F I L Q L K	89
CAG CTT CTT GCC TGT GGT AAT ACC AAG TTT GAG GCA TTG ACA GTT GTG ATT CAG	613
Q L L A C G N T K F E A L T V V I Q	107
CAC CTG CTG TCT GAG CGG GAG GAA GCA CTG AAA CAA CAC AAA ACC CTA TCT CAA	667
H L L S E R E E A L K Q H K T L S Q	125
1 GAA CTT GTT AAC CTC CGG GGA GAG CTA GTC ACT GCT TCA ACC ACC TGT GAG AAA	721
E L V N L R G E L V T A S T T C E K	143
TTA GAA AAA GCC AGG AAT GAG TTA CAA ACA GTG TAT GAA GCA TTC GTC CAG CAG	775
L E K A R N E L Q T V Y E A F V Q Q	161
CAC CAG GCT GAA AAA ACA GAA CGA GAG AAT CGG CTT AAA GAG TTT TAC ACC AGG	829
H Q A E K T E R E N R L K E F Y T R	179
GAG TAT GAA AAG CTT CGG GAC ACT TAC ATT GAA GAA GCA GAG AAG TAC AAA ATG	883
E Y E K L R D T Y I E E A E K Y K M	197
CAA TTG CAA GAG CAG TTT GAC AAC TTA AAT GCG CAT GAA ACC TCT AAG TTG GAA	937
Q L Q E Q F D N L N A H E T S K L E	215
2 ATT GAA GCT AGC CAC TCA GAG AAA CTT GAA TTG CTA AAG AAG GCC TAT GAA GCC	991
I E A S H S E K L E L L K K A Y E A	233
TCC CTT TCA GAA ATT AAG AAA GGC CAT GAA ATA GAA AAG AAA TCG CTT GAA GAT	1045
S L S E I K K G H E I E K K S L E D	251
TTA CTT TCT GAG AAG CAG GAA TCG CTA GAG AAG CAA ATC AAT GAT CTG AAG AGT	1099
L L S E K Q E S L E K Q I N D L K S	269
3 GAA AAT GAT GCT TTA AAT GAA AAA TTG AAA TCA GAA GAA CAA AAA AGA AGA GCA	1153
E N D A L N E K L K S E E Q K R R A	287
AGA GAA AAA GCA AAT TTG AAA AAT CCT CAG ATC ATG TAT CTA GAA CAG GAG TTA	1207
R E K A N L K N P Q I M Y L E Q E L	305

Figure 41



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GAA AGC CTG AAA GCT GTG TTA GAG ATC AAG AAT GAG AAA CTG CAT CAA CAG GAC	1261
E S L K A V L E I K N E K L H Q Q D	323
ATC AAG TTA ATG AAA ATG GAG AAA CTG GTG GAC AAC AAC ACA GCA TTG GTT GAC	1315
I K L M K M E K L V D N N T A L V D	341
AAA TTG AAG CGT TTC CAG CAG GAG AAT GAA GAA TTG AAA GCT CGG ATG GAC AAG	1369
K L K R F Q Q E N E E L K A R M D K	359
CAC ATG GCA ATC TCA AGG CAG CTT TCC ACG GAG CAG GCT GTT CTG CAA GAG TCG	1423
H M A I S R Q L S T E Q A V L Q E S	377
CTG GAG AAG GAG TCG AAA GTC AAC AAG CGA CTC TCT ATG GAA AAC GAG GAG CTT	1477
L E K E S K V N K R L S M E N E E L	395
CTG TGG AAA CTG CAC AAT GGG GAC CTG TGT AGC CCC AAG AGA TCC CCC ACA TCC	1531
L W K L H N G D L C S P K R S P T S	413
TCC GCC ATC CCT TTG CAG TCA CCA AGG AAT TCG GGC TCC TTC CCT AGC CCC AGC	1585
S A I P L Q S P R N S G S F P S P S	431
ATT TCA CCC AGA TGA cacgtccccaagtcacagactctctgaaagcattttgatgcaggtctgc	1651
I S P R *	436
aggactgaccccaaggaggaacgtgggcacaaagaggtatatcagcacacgtgtgatcaccgtaggtaactgg	1723
agcgctcaccaccggcggaatcgagcttctgagactggaagtctggaggaagacttttgcctccgtccaaaag	1795
attcctccaaaaaaagatttaaaaaaagatttcggcatcgacacggacgttggtgcacaaagcacttaaaaga	1867
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tataacctttgtaatgttcttcaccacagacaccttcttgtgagttttcagttctgactgtggtgggtggggg	2011
tgtgaatgaaatggatgtcacagagtgtcatgtgtctgatgcagcctcctctgctgtgtattaaatgtcaaa	2083
atctgaatatatctggatatgtactaatcaataataatcaatcaatcagcatatacatttcagccaaagcc	2155
atagaagaaaaagcaatagttgcttgaattatgatcatctaccaccaactctgctcagccctgtaacaggggt	2227
agggagaggggtataacaggaagagctttgacttgtccctgtctatacattctctgtatcttttgggggtaac	2299
ttcttggcagtttttcagtggttcagccatgtcagttgaaactagatttttctgtagattttttacttaccca	2371
tgtgagcctaactatctctgtaattcattttctcaggctatgtgtaaagtagaaccttaatttttctata	2443
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cctttgatctacccttgcagatttaacctgtcttcttccctccctatttctcattttccttttacctttct	2587
ccaccatccagagccacaaaagcaaaccttctacctcctacctacttttctctgggacaaggataaaggaat	2659
atgattttccagagccccagagccagctcatcttcagggtgctgaaaccactttccaaataaactaaagcct	2731
ggatttgatattacaaattttgggaaatcttagaataaagaacgagaacaaggaagtcattgggctagtataa	2803
ttaagaaaggtaggattcagtgcttaccgatgatgcagtacttgatagaagaaaacagtcctgggaggatagc	2875
gctcatttttcagttaccctttaaggagtcctttgtctttgggaaagtagcagaatgggtccgcttctttcc	2947
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**Figure 4.2**



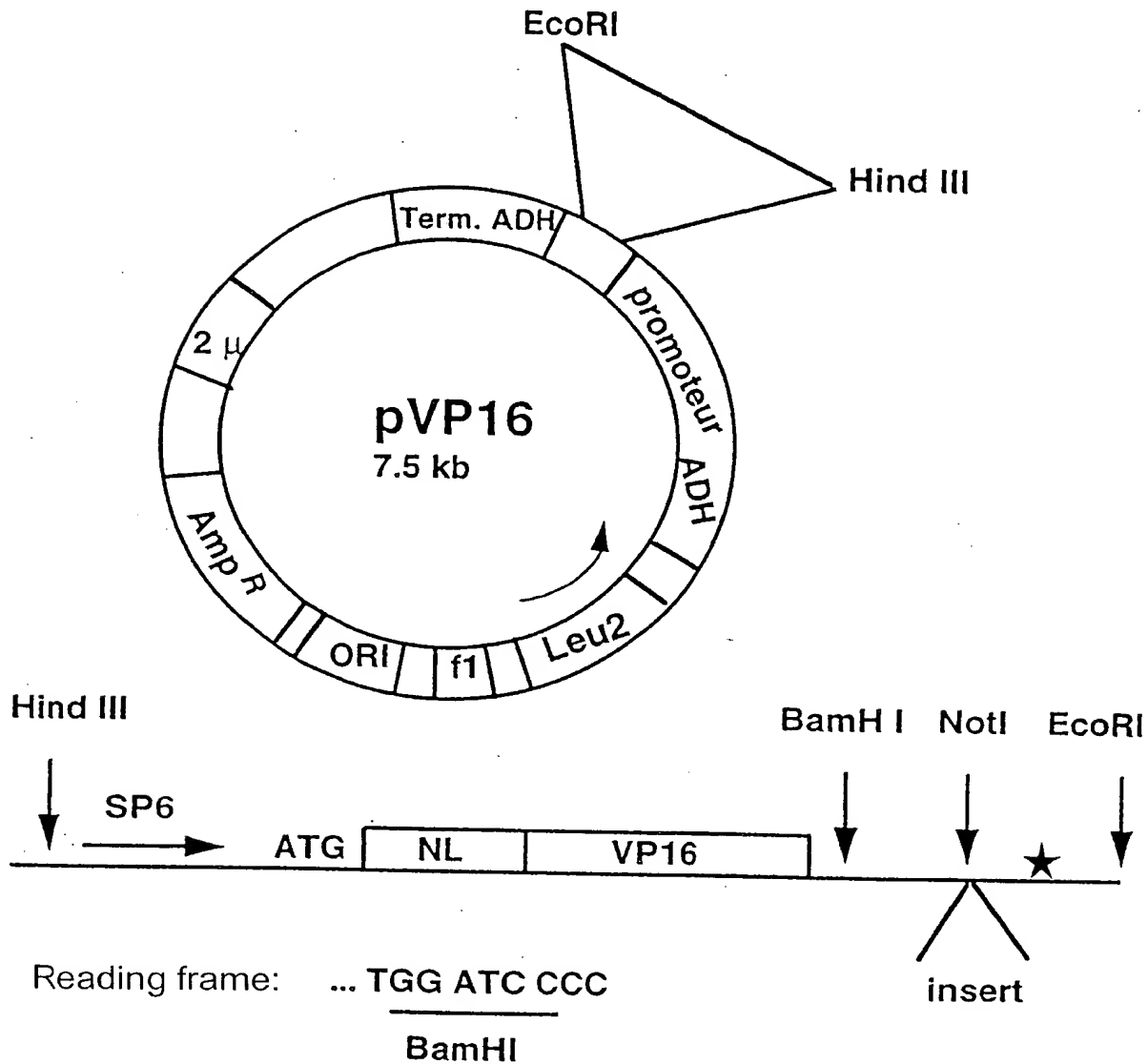
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tcccctaatacctgagactttggaaaaggtggaaggaagaactggttgctttatctccccctccctgcatgtgt 3091  
caacattgtgatgtcagatatttactaatctacattcagtggtgtgacaaataacagctgtagtaagaagaga 3163  
ttcaggatgctagaggtgaatatttgggtcatttacatgtacactacatagcaagttgatactcatgttgca 3235  
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cctgctgtcctccgtattacgtgaccggcaataaatctcatagcagttaatataaaacatctttggaggat 3523  
gggagagaacaggagggaagatgggaaacaaaatagagaattcttaagattttgtttaaaccaaatgtttca 3595  
tgtagaatgcaaaatgttggcacgtcaaaaatatgaatgtgtagacaactgtagttgtgctcagttttagt 3667  
gatgggaagtgtattttactctgatcaaataaataatgctggaatactcaaaaaaaaaaaaaaaaaaaaaa 3739  
aaa 3742

**Figure 4.3**



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★ Stop codons in three frames

pVP16 was constructed by Stan Hollenberg

Figure 5





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6 histidines

98.	ATG	CGG	GGT	TCT	CAT	CAT	CAT	CAT	CAT	GGT	ATG	
134	GCT	AGC	ATG	ACT	GGT	GGA	CAG	CAA	ATG	GGT	CGG	GAT
170	CTG	TAC	GAC	GAT	GAC	GAT	AAG	GAT	CGA	TGG	GGA	TCC
206	GAG	CTC	GAG	ATC	TGC	AGC	TGG	TAC	CAT	GGA	ATT	CGA
242	AGC	TTG	ATC	CGG	CTG	CTA	ACA	AAG	CCC	GAA	AGG	AAG
278	CTG	AGT	TGG	CTG	CCA	CCG	CTG	AGC	AAT	AAC	TAG...	

BamHI

Figure 6

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Tag Myc

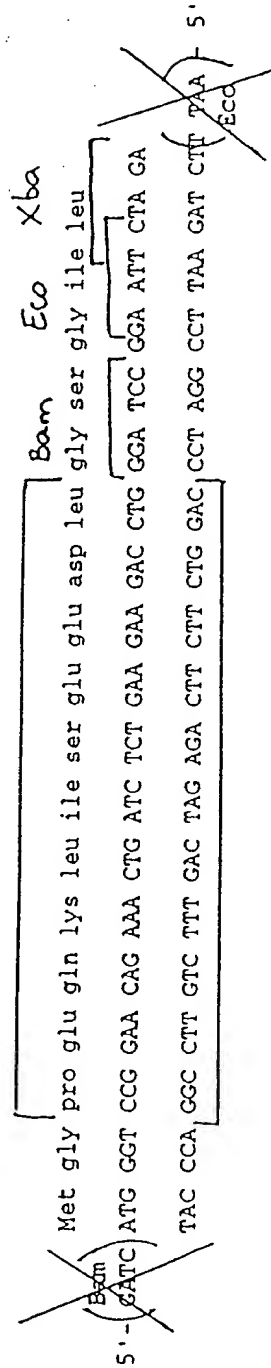
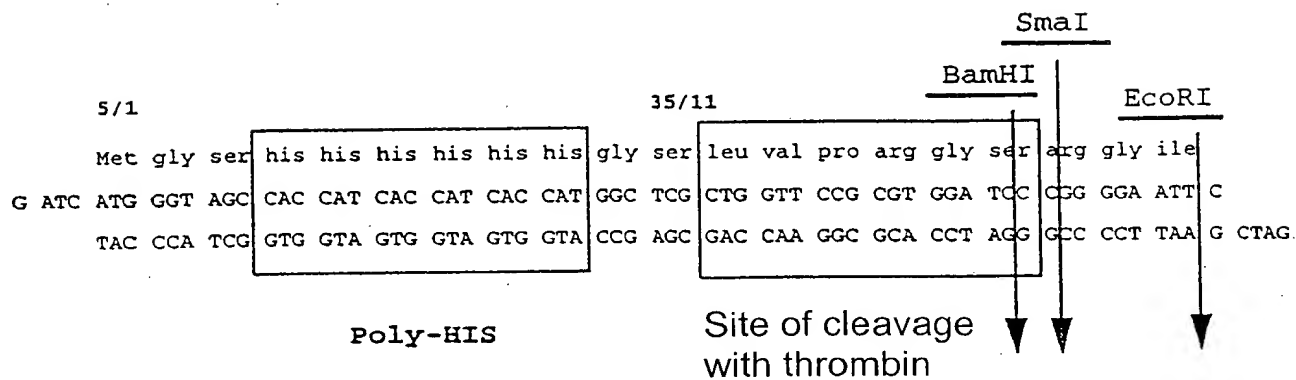


Figure 7



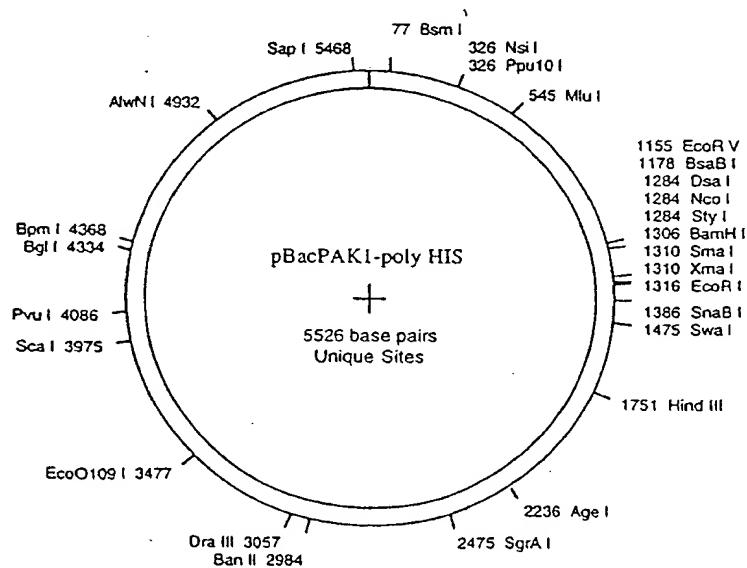
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pBacPAK1-poly HIS -> Graphic Map

DNA sequence 5526 b.p. AACGGCTCCGCC ... TCATTATGCAG circular

PolyHIS insertion into pBackpack in BamHI (CACCAT) 3 1270-1287



**Figure 8**



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Tissues:

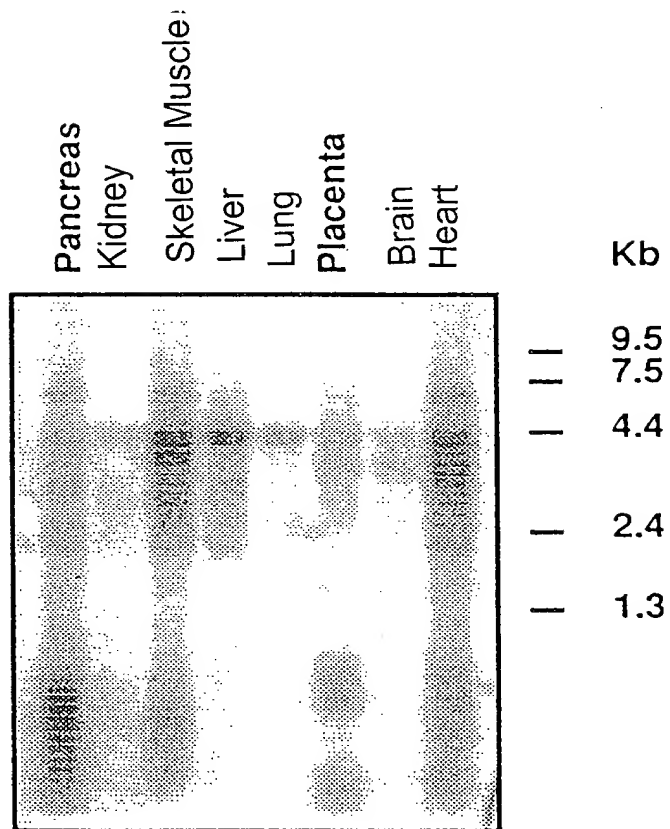


Figure 9

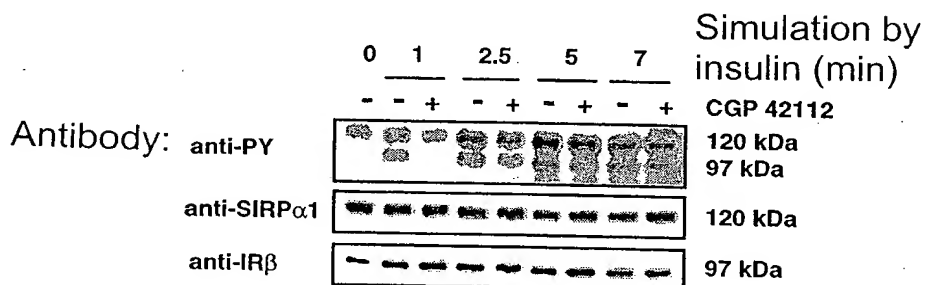
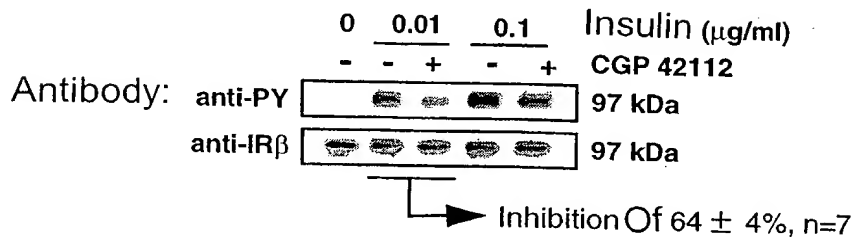




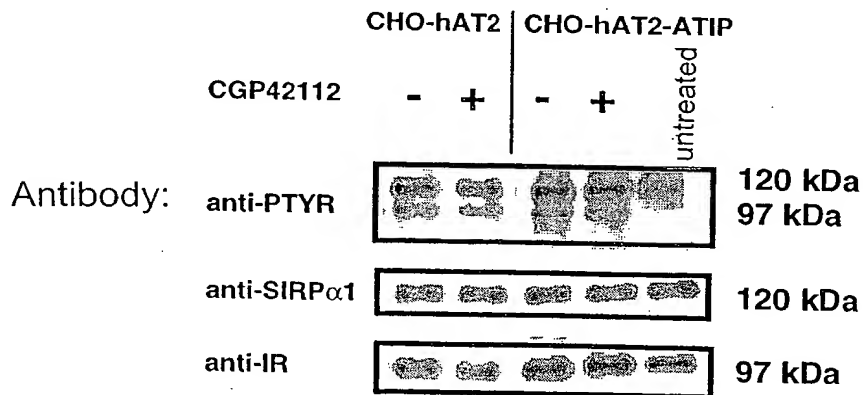
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## CHO-hAT2

### Lectin column



## CHO-hAT2 et CHO-hAT2-ATIP



**Figure 11**